

REMARKS

Applicants hereby submit that the enclosures fulfill the requirements under 37 C.F.R. §1.821-1.825. The amendments in the specification merely correct typographical errors and replace the original Sequence Listing with an amended substitute Sequence Listing wherein SEQ ID NOs:5, 6, 9 and 10 have been amended to reflect the nucleic acid and amino acid sequence disclosures described in the specification.

Paragraph [0242] describes the amino acid sequence of the invention, SEQ ID NO:10, as variations of the amino acid sequence depicted in SEQ ID NO:8 (Figure 8). Both sequences consist of 432 amino acid residues. Applicants inadvertently omitted amino acid residues 169 (Arginine) and 278 (Leucine) from the original Figure 8 of the instant application. Applicants submit herewith an amended substitute Figure 8 containing the amended SEQ ID NO:10. No new matter has been added.

Further, the amino acid variations described in paragraph [0242] are the result of nucleotide variations of SEQ ID NO:7 as described in paragraphs [0047], [0241], and [0246]. The nucleic acid sequence of the invention, SEQ ID NO:9, is erroneous as a result of a miscalculation of the nucleotides in SEQ ID NO:7. It is apparent that the miscalculation of the nucleotides in SEQ ID NO:7 led to the misnumbering of the nucleotide variations described in paragraphs [0047], [0241], and [0246]. For example, the combination of nucleotide variations "nucleotide 438 is T, 439 is G and 440 is G" provided in paragraphs [0047], [0241], and [0246] would result in Q84L and R85G in SEQ ID NO:10 instead of the variation Q84W intended for SEQ ID NO:10 provided in paragraph [0242] of the specification. By decreasing each of the nucleotide variations of SEQ ID NO:7 described in paragraphs [0047], [0241], and [0246] by one nucleotide (i.e., changing "nucleotide 438 is T" to "nucleotide 437 is T", and so forth) the nucleotide of the invention, SEQ ID NO:9, is achieved, which translates the amino acid sequence of the invention, SEQ ID NO:10, as described by the variations in paragraph [0242] of the specification. Therefore, each nucleotide variation described in paragraphs [0047], [0241] and [0246] have been decreased by one nucleotide as shown in the amendments to the specification, and the amended nucleic acid and amino acid sequences of the invention are provided in the substitute Sequence Listing as SEQ ID NOs:9 and 10, respectively.

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Further, the corrected nucleotide variations result in changes to SEQ ID NOs:5 and 6 in the original Sequence Listing. The substitute Sequence Listing contains the amended nucleic acid sequences in SEQ ID NOs:5 and 6 that coincide with the amended specification. No new matter has been added.

Attached hereto is a marked-up version of the changes made to the specification by the current amendment.

Please apply any charges or credits to Deposit Account No. 06-1050, referencing attorney docket number 09010-029006.

Respectfully submitted,

Date: Nov. 13, 2002

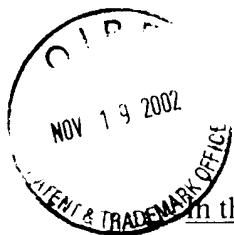


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"Version With Markings to Show Changes Made"

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in the specification:

Paragraph [0001] beginning at page 1, line 2, has been amended as follows:

This application is a continuation-in-part of U.S. Patent Application Serial No. 09/580,515, filed May 25, 2000, which is a continuation-in-part of U.S. Patent Application Serial No. 09/318,528, now U.S. Patent No. 6,183,740, filed May 25, 1999, which is a continuation-in-part of U.S. Patent Application Serial No. 09/291,931, now U.S. Patent No. 6,190,897, filed April 13, 1999, which is a continuation of U.S. Patent Application Serial No. 09/259,214, now U.S. Patent No. 6,110,719, filed March 1, 1999, which is a divisional of U.S. Patent Application Serial No. 08/910,798, now U.S. Patent No. 5,876,997, filed August 13, 1997, all of which are hereby incorporated by reference in their entirety.

Paragraph [0047] beginning at page 14, line 9, has been amended as follows:

The invention also provides phytase encoding polynucleotides having a nucleotide sequence substantially identical to SEQ ID NO:7, and having a modified nucleotide sequence selected from nucleotide [390] 389 is G; [391] 390 is A; nucleotide [438] 437 is T; [439] 438 is G; [440] 439 is G; [471] 470 is C; [473] 472 is T; [477] 476 is T; [448] 477 is G; [449] 478 is T; [690] 689 is G; [691] 690 is A; [692] 691 is G; [729] 728 is T; [730] 729 is A; [731] 730 is T; [864] 863 is T; [865] 864 is G; [1017] 1016 is G, or any combination thereof. Further, the invention provides a polynucleotide having a nucleotide sequence substantially identical to SEQ ID NO:7, and having a modified nucleotide sequence selected from nucleotide [390] 389 is G and [391] 390 is A (SEQ ID NO:5); nucleotide [438] 437 is T, [439] 438 is G and [440] 439 is G (SEQ ID NO:6); [471] 470 is C and [473] 472 is T; [477] 476 is T, [448] 477 is G, and [449] 478 is T; [690] 689 is G, [691] 690 is A and [692] 691 is G; [729] 728 is T, [730] 729 is A, and [731] 730 is T; [864] 863 is T and [865] 864 is G; [1017] 1016 is G, or any combination thereof. The later sequence is exemplified in SEQ ID NO:9 and the corresponding amino acid sequence is SEQ ID NO:10.

Paragraph [0056] beginning at page 15, line 22, has been amended as follows:

Figures 7A and 7B shows the nucleotide sequence of E. coli appA phytase (SEQ ID NO:7).

Paragraph [0241] beginning at page 73, line 6, has been amended as follows:

Examples of a variant phytase polynucleotide sequence include sequences substantially as set forth in SEQ ID NO:7, wherein the polynucleotide has a nucleotide sequence as set forth in a) SEQ ID NO:9; b) SEQ ID NO:9 wherein all Ts are Us (RNA); wherein the expression of the phytase-encoding nucleic acid leads to the production of said substantially pure phytase enzyme; and c) SEQ ID NO:7, wherein [390] 389 is G; [391] 390 is A (SEQ ID NO:5); nucleotide [438] 437 is T; [439] 438 is G; [440] 439 is G (SEQ ID NO:6); [471] 470 is C; [473] 427 is T; [477] 476 is T; [448] 477 is G; [449] 478 is T; [690] 689 is G; [691] 690 is A; [692] 691 is G; [729] 728 is T; [730] 729 is A; [731] 730 is T; [864] 863 is T; [865] 864 is G; [1017] 1016 is G, or any combination thereof. More specifically, with respect to part c), the invention provides a nucleotide sequence substantially identical to SEQ ID NO:7, and having a modified nucleotide sequence selected from nucleotide [390] 389 is G and [391] 390 is A; nucleotide [438] 437 is T, [439] 438 is G and [440] 439 is G; [471] 470 is C and [473] 472 is T; [477] 476 is T, [448] 477 is G, and [449] 478 is T; [690] 689 is G, [691] 690 is A and [692] 691 is G; [729] 728 is T, [730] 729 is A, and [731] 730 is T; [864] 863 is T and [865] 864 is G; [1017] 1016 is G, or any combination thereof.

Paragraph [0242] beginning at page 73, line 19, has been amended as follows:

Examples of a variant phytase polynucleotide of the invention also include a polynucleotide that encodes a polypeptide having substantially as set forth in SEQ ID NO:8, but having an W68E, Q84W, A95P, K97C, S168E, [R180Y] R181Y, N226C, Y277D or any combination thereof and retain phytase activity.

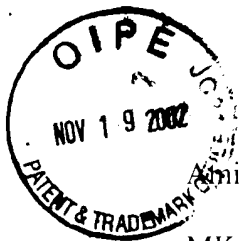
Paragraph [0246] beginning at page 75, line 10, has been amended as follows:

An oligonucleotide of the invention can include a portion of a phytase polynucleotide, including, for example, a sequence substantially identical to that of SEQ ID NO:7, except

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wherein nucleotide wherein [390] 389 is G; [391] 390 is A; nucleotide [438] 437 is T; [439] 438 is G; [440] 439 is G; [471] 470 is C; [473] 427 is T; [477] 476 is T; [448] 477 is G; [449] 478 is T; [690] 689 is G; [691] 690 is A; [692] 691 is G; [729] 728 is T; [730] 729 is A; [731] 730 is T; [864] 863 is T; [865] 864 is G; [1017] 1016 is G, or wherein the oligonucleotide contains a combination of such substitutions with respect to SEQ ID NO:7. Thus, as disclosed herein, the oligonucleotide can be any length and can encompass one or more of the above mutations.



Amino acid sequence for E. coli appA (wild type) (SEQ ID NO:8)

MKAILIPFLSLLIPLTPQSAFAQSEPELKLESVVIVSRHGVRAPTKATQLMQDVTP
DAWPTWPVKLG**W**LTPRGGELIAYLGHY**Q**RQRLVADGLL**A****K**KGCPQSGQVAIIA
DVDERTRKTEGAFAAGLAPDCAITVHTQADTSSPDPLFNPLKTGVCQLDNA
NVTDAIL**S**RAGGSIADFTGH**R**QTAFRELERVLNFPQSNLCLKREKQDESCSLTQA
LPSELKVSAD**N**VSLTGAVSLASMLTEIFLLQQAQGMPEPGWGRITDSHQWNTLL
SLHNAQF**Y**LLQRTPEVARSRATPLLDLIKALTTPHPPQKQAYGVTLPSTVLFIAHG
DTNLANLGGALELNWTLPGQPDNTPPGGELVFERWRRLSDNSQWIVSLVFQTL
QQMRDKTPLSLNTPPGEVKLTLAGCEERNAQGMCSLAGFTQIVNEARIPACSL

Bold-Underlined amino acid residues are shown below in the modified appA enzyme
(SEQ ID NO:10)

MKAILIPFLSLLIPLTPQSAFAQSEPELKLESVVIVSRHGVRAPTKATQLMQDVTP
DAWPTWPVKLG**E**RLTPRGGELIAYLGHY**W**RQRLVADGLL**P****C**KGCPQSGQVAII
ADVDERTRKTGEAFAAGLAPDCAITVHTQADTSSPDPLFNPLKTGVCQLDNA
NVTDAILE**A**AGGSIADFTGH**Y**QTAFRELERVLNFPQSNLCLKREKQDESCSLTQAL
PSELKVSAD**C**VSLTGAVSLASMLTEIFLLQQAQGMPEPGWGRITDSHQWNTLLS
LHNAQF**D**LLQRTPEVARSRATPLLDLIKALTTPHPPQKQAYGVTLPSTVLFIAHG
DTNLANLGGALELNWTLPGQPDNTPPGGELVFERWRRLSDNSQWIVSLVFQTL
QQMRDKTPLSLNTPPGEVKLTLAGCEERNAQGMCSLAGFTQIVNEARIPACSLRS
HL

Figure 8

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